

#5

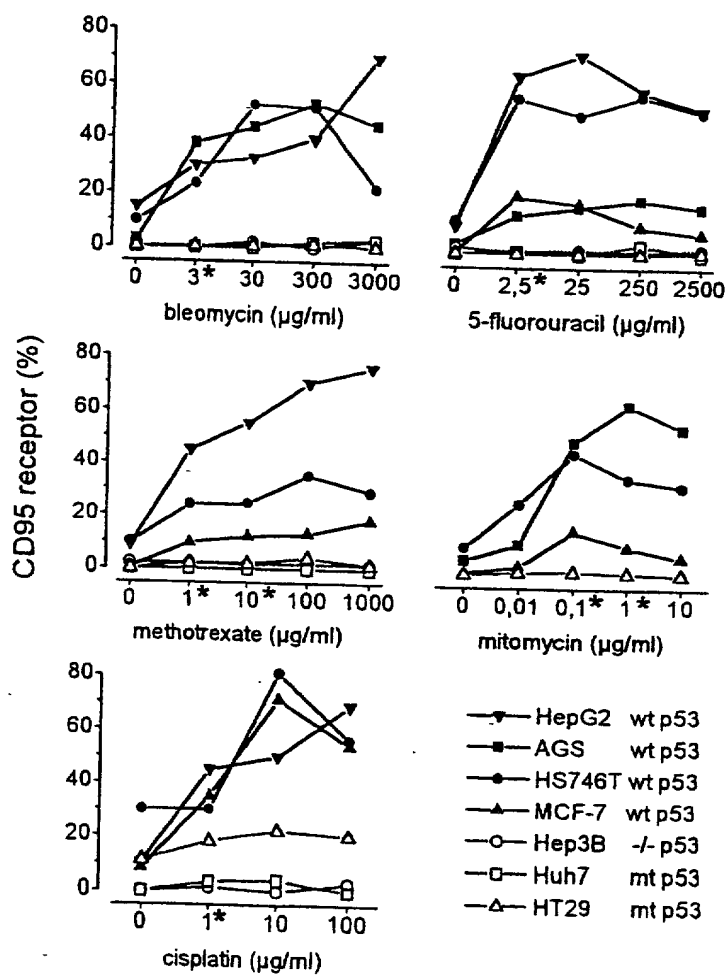


Fig. 1

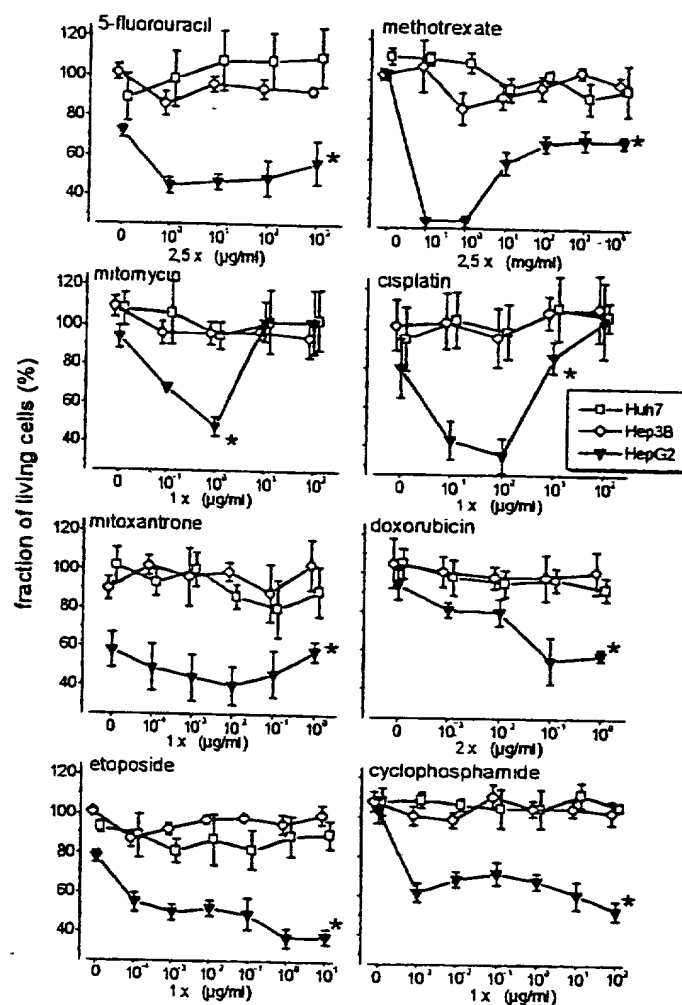


Fig. 2

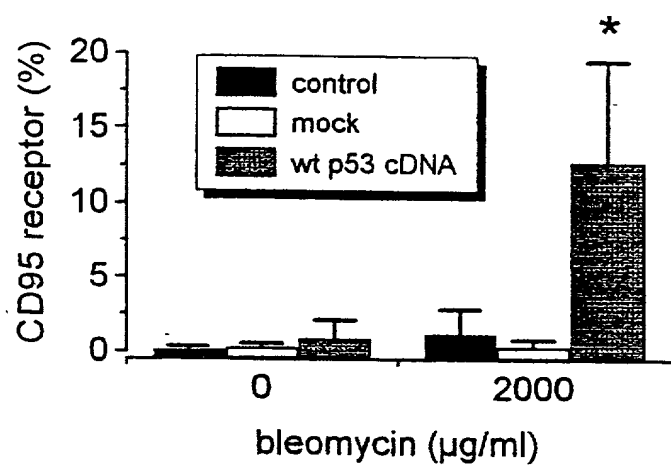


Fig. 3

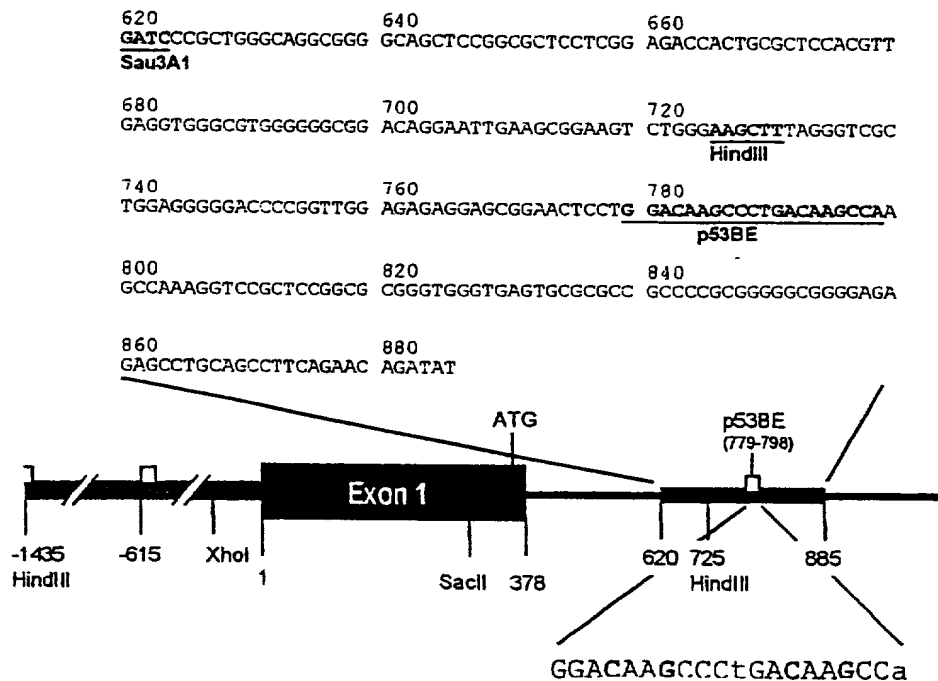


Fig. 4

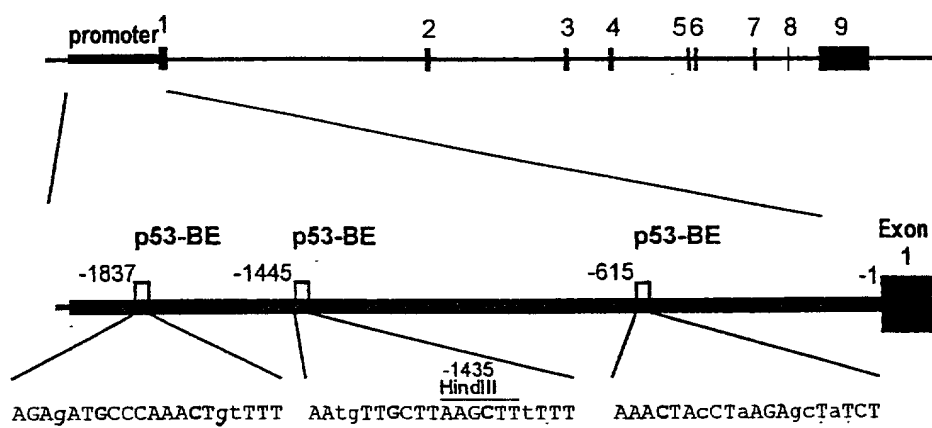


Fig. 5

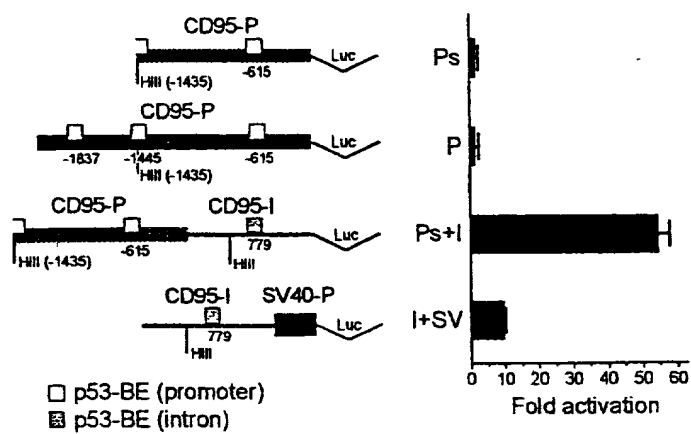


Fig. 6

GATCCCGCTGGGCAGGCGGGGCAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTT
 1 -----+-----+-----+-----+-----+ 60
 CTAGGCGGACCCGCTCCGCCCCGTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAA

 GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGC
 61 -----+-----+-----+-----+-----+ 120
 CTCCACCCGACCCCCCGCTGTCTTAACTTCGCCTTCAGACCTTCGAAATCCCAGCG

 <---- 4. P53-BE ---->
 (intron)
 TGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAA
 121 -----+-----+-----+-----+-----+ 180
 ACCTCCCCCTGGGGCCAACCTCTCTCTCGCCTTGAGGACCTGTTGGGACTGTTGCGGT

 GCCAAAGGTCCGCTCCGGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGCGGGGAGA
 181 -----+-----+-----+-----+-----+ 240
 CGGTTTCCAGGCGAGGCCGCGCCACCCACTCACGCGCGGGCGGGGCGCCCCGCCCCCTCT

 GAGCCTACAGCCTTCAGAACACATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAA
 241 -----+-----+-----+-----+-----+ 300
 CTCGGATGTCGGAAGTCTTGTGTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTT

 TAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTT
 301 -----+-----+-----+-----+-----+ 360
 ATTCAGTCGTGGCTTCGTACCAATTCCGGCTCCCGAGCCTTCTTGCCGTGGAAAAGAAA

 CTCGAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATT
 361 -----+-----+-----+-----+-----+ 420
 GAGCTTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAA

 GTCACACAGAAAAGGAAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAAGACTGTA
 421 -----+-----+-----+-----+-----+ 480
 CAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATTCTGACAT

 AGTCGCTGCCTGAGTGGTTTCATTTTGTTTTGTCTTCTGCCCTTCTCTTTCTTTTGG
 481 -----+-----+-----+-----+-----+ 540
 TCAGCGACGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAC

 CCCTTTCTTAGCTTGCCTCCCATGGTGATTCTGCTTGGTCTCCTGCTGGGGTTGGTGG
 541 -----+-----+-----+-----+-----+ 600
 GGGAAAGAATCGAACGTGAGGGTACCACTAAAGACGAACCAGAGGACGACCCCAACCACC

 TACTCGTTCACCCGACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCT
 601 -----+-----+-----+-----+-----+ 660
 ATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGTTCTTTGAACTCGTCGGA

 GTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGACAGATGGCTAATCAAAGAGACGTG
 661 -----+-----+-----+-----+-----+ 720
 CAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTCTCTGCAC

Fig. 7

2nd half of the
2.p53-BE
(promoter)

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AGCTTTTTTGGCTACATTTTTTTATTGTAAAG
448 -----+----- 480
TCGAAAAAACCGATGTAAAAAATAAACATTC

TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
481 -----+----- 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTATAATTCAATTCCTTCTAG

CACATATGTGAGTTGCTGGCTTATAATTCACTCAAGAGATACTGATTTTGTCAATTGT
541 -----+----- 600
GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAACAGTTAACA

CCTTCCCTTTTTTTCTCTCTCCCTCCCTCCATTCTTCTCCCTTACCTCTCCTTTC
601 -----+----- 660
GGAAAGGGGAAAAAAGAGAGAGGGGAGGAAGGTAAGGAAGGAATGGAGAGGAAAG

CTTCCCTCACACCCCTTTTCCCTTCTTTTACATTTTTTTATTAAATGAACTTTTC
661 -----+----- 720
GAAGGGAGTGTGGGGAAGGAAGGAAGAAATGTAAAAAATAAATTTACTTGAAAAG

ATTTTGGATAGTTTTAGGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA
721 -----+----- 780
TAAACCTTATCAAAATCCTAAAGTTTTTAACGTCCTATTATGTCTCTTACGGGTAT

TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
781 -----+----- 840
ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGT

GGCTGGCAGCCCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAGGTGGAACAGAG
841 -----+----- 900
CCGACCGTGCGGGTCCAGAAGGAGTACCGTGATTGTGAGATGACTTTCCACCTTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAAGTGACAGATGCAAAACACAGG
901 -----+----- 960
TGTTCCGATAGTTGTGGATGTTCTGACCACCATTCACGTCACTGTCTACGTTTGTGTCC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAACAGGCTCCA
991 -----+----- 1020
CACTACCTTTCGGGAGTCTCCCATTTGGATCTAAACTCCCGGGTTTGTCCGAGGT

GAAGAAAATGTCACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
1021 -----+----- 1080
CTTCTTTACAGTTGACTCTCTTCGGACTTCCTACTTGTACCCGATTCGTTTCCCAAT

```

Fig. 8A


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TTAATGTGTATTAAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
1081 -----+-----+-----+-----+-----+ 1140
AATTACACAATAATTACCCAACCTTAGATTAACCCCTCCCTCTCTCCAACGTCTCACTCCA

GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
1141 -----+-----+-----+-----+-----+ 1200
CGTCTCGAACCACCTGCTACGGTTTCCTTATGACTTTGGAAATCACACAGGTCAGACCTT

CTGCATCCAAATTCAGGTTTCAGTAATGATGTCATTATCCAAACATACCTTCTGTAAAT
1201 -----+-----+-----+-----+-----+ 1260
GACGTAGGTTTAAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

      <--- 3.p53-BE --->
      (promoter)

CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
1261 -----+-----+-----+-----+-----+ 1320
GTACGATTGTGGAATCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCAACA

TCACCAGAGCACGAAAGAATTACAAGATTTTTTTTAAAGAAAATTGGCCAGGAAATAAT
1321 -----+-----+-----+-----+-----+ 1380
AGTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCTTTATTA

GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGGCTATGCGATTTG
1381 -----+-----+-----+-----+-----+ 1440
CTCATTGTCTTCCTGTCCTTCATTAAACATTACAAATTATATCGACCCCGATACGCTAAAC

GCTTAAGTTGTAGCTTTGTTCCTCTTGAGAAATAAAAACTAAGGGGCCCTCCCTTTT
1441 -----+-----+-----+-----+-----+ 1500
CGAATTCAACAATCGAAACAAAGGAGAACTCTTTATTTTGTATCCCGGGAGGAAAAA

CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
1501 -----+-----+-----+-----+-----+ 1560
GTCTCGGGATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

GTCTGTGAGCCTCTCATGTTGCAGCCACAACATGGACAGCCAGTCAAATGCCCGCAG
1561 -----+-----+-----+-----+-----+ 1620
CAGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTCCGGTCAGTTTACGGGGCGTTC

TCTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC
1621 -----+-----+-----+-----+-----+ 1680
AGAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGAGC

GCTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTTCCAGGTTGAACTACAGCAGAA
1681 -----+-----+-----+-----+-----+ 1740
CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGGTCCAACCTTGATGTCGTCTT

GCCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGC
1741 -----+-----+-----+-----+-----+ 1800
CGGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGAGTTCACCTCGTACGGTGC

CACTGCAGGAACGCCCGGGACAGGAATGCCCATTTGTGCAACGAACCTGACTCCTTCC
1801 -----+-----+-----+-----+-----+ 1860
GTGACGTCCTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGG

TCACCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC
1861 -----+-----+-----+-----+-----+ 1920
AGTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGTTCAACGACTTAGTTACCTCG

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Fig. 8B

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CCTCCCCAACCCGGGGCTTCCCCAGCGAGGCTTCTTCCCATCTCTGACCACCGGGG
1921 -----+-----+-----+-----+-----+ 1980
GGAGGGGTGGGCCCCGAAGGGTCTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT
1981 -----+-----+-----+-----+-----+ 2040
AAAAGCACTCGAGCAGAGACTAGAGCGGCTTCTCACTGTGTGTCCACAAGTTTCTGCGAA

CTGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTG
2041 -----+-----+-----+-----+-----+ 2100
GACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCGCCCGTGAC

GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGTGCCTCTTCTCCCGC
2101 -----+-----+-----+-----+-----+ 2160
CGTGCCCTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCCTCGACGGAGAAGAGGGCG

GGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCGGTGCACCTTAAGCTTTA
2161 -----+-----+-----+-----+-----+ 2220
CCTGTACATGTCTCGAGCTCTTATGATCACCAGGTGCACCCGGCACGTGGAATTCGAAAT

                                     ←---4.p53-BE-
                                     (intron)

GGGTCGCTGGAGGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTCGACAAGCCCTGAC
2221 -----+-----+-----+-----+-----+ 2280
CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCTCGCCTTGAGGACCTGTTCCGGGACTG

-----→

AAGCCAAGCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCGCGCCGCCCGCGGGGGC
2281 -----+-----+-----+-----+-----+ 2340
TTCCGTTTCGGTTTCCAGGCGAGGCGCGCCACCCACTCAGCGCGGGCGGGCGCCCCCG

GGGAGAGAGCCTGCAGCCTTCAGAACAGATATGCTCATTCTTCTGGCAGTTCTCAGACG
2341 -----+-----+-----+-----+-----+ 2400
CCCCCTCTCTCGGACGTCCGGAAGTCTTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC

TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
2401 -----+-----+-----+-----+-----+ 2460
ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA

TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
2461 -----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

TTTTATTGTACACAGAAAAGGAACTGCCTTGTCTCCCTTCCGGGAATTCTCTCTTTAA
2521 -----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCTTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATT

GACTGTAAAGTCGCTGCCTGAGTGGTTTCATTTTGTTTTGTCTTCTGCCCTTCTCTTTCT
2581 -----+-----+-----+-----+-----+ 2640
CTGACATTTCAGCGACGGACTCACCRAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

TCTTTTGCCCTTTCTTAGCTTGCACCTCCCATGGTGATTTCTGCTTGGTCTCCTGTGGGG
2641 -----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAGAATCGAACGTGAGGGTACCCTAAAGACGAACCAAGAGGACGACCCC

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Fig. 8C

TTGGTGGTACTCGTTCCCAACCGCACAGAACCCGGCGCCTATTATTGGCCAAGAACTTGA
 2701 -----+-----+-----+-----+-----+ 2760
 AACCACCATGAGCAAGGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT

 GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGCAGATGGCTAATCAAAG
 2761 -----+-----+-----+-----+-----+ 2820
 CGTCGGACAAAACCTTTTCAGGGAGCGAGTCTTTACGGTCGAACGTCTACCGATTAGTTTC

 AGACGTG
 2821 ----- 2827
 TCTGCAC

Fig. 8D

<---- 1.p53-BE --

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1  TGAGGACTCTCAGGAATATGCTGGTAAATATAAATAACCTTTAGAGATGCCCAAACGT
  -----+-----+-----+-----+-----+-----+
60  ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTGACA
  -----+-----+-----+-----+-----+-----+

-->

61  TTCCCCAGAACACCAGCATTATTAGGTGTTCAATCAATAGATTCTTCAAAGGATTCCA
  -----+-----+-----+-----+-----+-----+
120  AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTTCTAAGGT
  -----+-----+-----+-----+-----+-----+

121  AAGGCAAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCTTTGACATTAGCATAC
  -----+-----+-----+-----+-----+-----+
180  TTCCGTTTCTTCAAACCCCTTGTATATATATTAATGGGTGGGAACTGTAATCGTATG
  -----+-----+-----+-----+-----+-----+

181  TAAGGGCCCTGAGAAGTTTGGATTAAAGAAAGTTTCAAATTAAGTAACCCAGAATTTT
  -----+-----+-----+-----+-----+-----+
240  ATTCCTGGGACTCTTCAAACCTAATCTTTCAAAGTTTAATTTTATTGGGTCTTAAAA
  -----+-----+-----+-----+-----+-----+

241  CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCACATATTCCTATCTCCTT
  -----+-----+-----+-----+-----+-----+
300  GATTCTAATAAATGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
  -----+-----+-----+-----+-----+-----+

301  GAACCTGAGGATAATTAGACGTACGTGGGTAGAGGTAGGGGAAGGGGGTATGGCATAGA
  -----+-----+-----+-----+-----+-----+
360  CTTGAACCTCTATTAATCTGCATGCACCCATCTCCCATCCCTTCCCCCATACCGTATCT
  -----+-----+-----+-----+-----+-----+

361  AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA
  -----+-----+-----+-----+-----+-----+
420  TTCTCGTCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT
  -----+-----+-----+-----+-----+-----+

<---- 2.p53-BE ---->

421  ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTTATTGTAAAG
  -----+-----+-----+-----+-----+-----+
480  TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTTT
  -----+-----+-----+-----+-----+-----+

481  TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC
  -----+-----+-----+-----+-----+-----+
540  ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTATAATTCATTCTCTTAG
  -----+-----+-----+-----+-----+-----+

541  CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGATACTGATTTTGTCAATTGT
  -----+-----+-----+-----+-----+-----+
600  GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
  -----+-----+-----+-----+-----+-----+

601  CCTTTCCCTTTTTTTCTCTCTTCCCTCCTTCCATTCTTCTTCCCTTACCTCTCCTTTC
  -----+-----+-----+-----+-----+-----+
660  GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGAATGGAGAGGAAAG
  -----+-----+-----+-----+-----+-----+

```

Fig. 9A

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661  CTTCCTCACACCCCTTTCTCCTTCTTTTACATTTTTTTATTAAATGAACTTTTTC
-----+-----+-----+-----+-----+-----+-----+
720  GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTTACTTGAAAAG

721  ATTTTGAATAGTTTTAGGATTTCAAAAAATTTGCAGAGATAATACAGAGAATGCCATA
-----+-----+-----+-----+-----+-----+-----+
780  TAAACCTTATCAAAATCCTAAAGTTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

781  TACCATCCTCCTTATCCCACTTCTTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
-----+-----+-----+-----+-----+-----+-----+
840  ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT

841  GGCTGGCAGCGCCAGGGTCTTCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
-----+-----+-----+-----+-----+-----+-----+
900  CCGACCGTGGCGGTCCAGAGGAGTACCGTGATTGTCAGATGACTTTCCACCTTGTCTC

901  ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
-----+-----+-----+-----+-----+-----+-----+
960  TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACGTCAGTGTCTACGTTTTGTGTCC

991  GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTTGAGGGCCCAAACAGGCTCCA
-----+-----+-----+-----+-----+-----+-----+
1020  CACTACCTTTCCGGAGTCTCCCATTTGGATTGGATCTAAACTCCCGGTTTGTCCGAGGT

1021  GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTA
-----+-----+-----+-----+-----+-----+-----+
1080  CTCTTTTACAGTTGACTCTCCTTCGGACTTCTTACTTGTACCCGATTCTGTTTCCCAAT

1081  TTAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGT
-----+-----+-----+-----+-----+-----+-----+
1140  AATTACACAATAATTACCCAATTAGATTAAACCTTCCCTCTCTCCAACGTCTCACTCCA

1141  GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAA
-----+-----+-----+-----+-----+-----+-----+
1200  CGTCTCGAACCACCTGTCTACGGTTTCTTATGACTTTGGAAATCACACAGGTGAGACCTT

1201  CTGCATCCAAATTCAGGTTTCAATGATGTCTATTATCCAAACATACCTTCTGTAAATTT
-----+-----+-----+-----+-----+-----+-----+
1260  GACGTAGGTTTAAAGTCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAA

<--- 3.p53-BE --->

1261  CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGACTTTGAACAGTGT
-----+-----+-----+-----+-----+-----+-----+
1320  GTACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTCAAC

1321  TCACCAGAGCACGAAAGAAATTACAAGATTTTTTTTTAAAGAAAATTGCCAGGAAATAAT
-----+-----+-----+-----+-----+-----+-----+
1380  AGTGGTCTCGTGCTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCTTTATTA

1381  GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAAATAGCTGGGGCTATGCGATTTG
-----+-----+-----+-----+-----+-----+-----+
1440  CTCATTGCTTCCTGTCCTTCATTAACTTACAAATTATATCGACCCCGATACGCTAAAC

1441  GCTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTT
-----+-----+-----+-----+-----+-----+-----+
1500  CGAATTCAACAATCGAAACAAAAGGAGAACTCTTTATTTTGATTCCCGGGAGGGAAAA

1501  CAGAGCCCTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCCAGGAAC
-----+-----+-----+-----+-----+-----+-----+
1560  GTCTCGGGATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCCTTG

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Fig. 9B


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TAGGAAATAAGTCAGCACCGAAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
2401 -----+-----+-----+-----+-----+ 2460
ATCCTTTATTTCAGTCGTGGCTTCGTACCAATTCGGCCTCCCGAGCCTTCTTGCCGTGGA

TTTCTTTCTCGAAAAAGTTATATGGGGGCTGAATGAGCTTCTGGAGGCTTGTTTACCGTT
2461 -----+-----+-----+-----+-----+ 2520
AAAGAAAGAGCTTTTTCAATATACCCCGACTTACTCGAAGACCTCCGAACAAATGGCAA

TTTTATTGTCACACAGAAAAGGAACTGCCTTGCTCCCTTCGGGAATTCTCTCTTTAA
2521 -----+-----+-----+-----+-----+ 2580
AAAATAACAGTGTGTCTTTTCCTTGACGGAACAGAGGGAAGGCCCTTAAGAGAGAAATT

GACTGTAAGTCGCTGCCTGAGTGGTTTCATTTTGTGTTTTCTGCCCTTCTCTTTCT
2581 -----+-----+-----+-----+-----+ 2640
CTGACATTTCAGCGACGGACTCACCAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

TCTTTTGCCCTTTCTTAGCTTGCACTCCCATGGTGATTTCTGCTTGGTCTCCTGCTGGGG
2641 -----+-----+-----+-----+-----+ 2700
AGAAAACGGGAAAGATCGAACGTGAGGGTACCCTAAAGACGAACCAGAGGACGACCCC

TTGGTGGTACTCGTTCCACCGCACAGAACCCGGCGCTATTATTGGCCAAGAACTTGA
2701 -----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGTGGCGTGTCTTGGGCCGCGGATAATAACCGGTTCTTTGAACT

GCAGCCTGTTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTTGAGATGGCTAATCAAAG
2761 -----+-----+-----+-----+-----+ 2820
CGTCGGACAAAACTTTTAGGGAGCGAGTCTTTACGGTCGAACGCTTACCGATTAGTTTC

AGACGTG
2821 ----- 2827
TCTGCAC

```

Fig. 9D

<---- 1.p53-BE ---->
(promoter)

1 TGAGGACTCTCAGGAATATGCTGGTAAAAATAAAATAACCTTTAGAGATGCCCAAACGTG 60
 ACTCCTGAGAGTCCTTATACGACCATTTTATTTTATTGGAAATCTCTACGGGTTTGACA
 -->

61 TTCCCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTTCAAAGGATTCCA 120
 AAAGGGGTCTTGTGGTCGTAAGTAATCCACAAGTAAGTATCTAAGAAGTTTCTTAAGGT
 121 AAGGCBAAGAAGTTTGGGGAACAGTATATATAATTACCCAACCCCTTTGACATTAGCATAC 180
 TTCCGPTTCTTCAAACCCCTTGTCTATATATTAATGGGTGGGAACTGTAATCGTATG
 181 TAAGGGCCCTGAGAAGTTTGGATTAAAGAAAGTTTCAAATTAAAGTAACCCAGAATTTT 240
 ATTCCCGGGACTCTTCAAACCTAATTCTTTCAAAGTTTAATTTCAATTGGGTCTTAAAA
 241 CTAAGATTATTTGACCATGAAACATATGTCTCCCCACAAAGCAGATATTCCTATCTCCTT 300
 GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTTCGTGTATAAGGATAGAGGAA
 301 GAACTTGAGGATAAATTAGACGTACGTGGGTAGAGGTAGGGGAAGGGGGTATGGCATAGA 360
 CTTGAACTCCTATTAACTGTCATGCACCCATCTCCCATCCCCCTCCCCCATACCGTATCT
 361 AAGAGCAGGACCTTGGGAGCAAGAATATCTAAGTTTAATTCCTGACTCTGCTATTTATTA 420
 TTCTCGTCCTGGAACCCCTCGTTCTTATAGATTCAAATTAAGGACTGAGACGATAAATAAT

<---- 2.p53-BE ---->
(promoter)

421 ACTAACCATCTTTGCCAATGTTGCTTAAGCTTTTTTGGCTACATTTTTTTATTGTAAAG 480
 TGATTGGTAGAAACGGTTACAACGAATTCGAAAAAACCGATGTAAAAAATAAACATTC
 481 TAAGTTTAATAATCACTCATCTCACTGGGCTATAATGATAAGTATTAAGTAAGGAAGATC 540
 ATTCAAATTATTAGTGAGTAGAGTGACCGATATTACTATTCTAATTCATTCTCTCTAG
 541 CACATATGTGAGTTGCTGGCTTATAATTCACACTCAAGAGTACTGATTTTGTCAATTGT 600
 GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTCTATGACTAAAACAGTTAACA
 601 CCTTTCCCTTTTTTCTCTCTTCCCTCCTTCCATTCTCTTCCCTTACCTCTCCTTTC 660
 GGAAAGGGGAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAATGGAGAGGAAG
 661 CTTCCCTCACACCCCTTTTCTCTCTTCTTTTACATTTTTTTATTTAAATGAACCTTTTC 720
 GAAGGGAGTGTGGGGAAAAGGAAGGAAGAAAATGTAAAAAATAAATTTACTTGAAAAG
 721 ATTTTGAATAGTTTGTAGGATTTCAAATAATTTGCAGAGATAATACAGAGAATGCCCAT 780
 TAAACCTTATCAAATCCTAAAGTTTTTAAACGTCTCTATTATGTCTCTTACGGGTAT

Fig. 10A


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      TACCATCCTCCTTATCCCACTTCTTTTGTGTCTATTAGATGCTCAGAGTGTGTGCACAA
781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
      ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

      GGCTGGCAGCCCCAGGGTCTTCCTCATGGCACAACAGTCTACTGAAAGGTGGAACAGAG
841 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
      CCGACCGTGCGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTTCACCTTGTCTC

      ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
901 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
      TGTTCGGATAGTTGTGGATGTTCTGACCACCATTACAGTCACTGTCTACGTTTGTGTCC

      GTGATGGAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCCAACAGGCTCCAG
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020
      CACTACCTTTCGGGAGTCTCTCCATTGGATTGGATCTAACTCCCGGGTTGTCCGAGGTC

      AAGAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGGCTAAGCAAAGGGTTAT
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080
      TTCTTTTACAGTTGACTCTCCTTCGACTTCCTACTTGTCAACCGATTGCTTTCCCAATA

      TAATGTGTTATTAATGGGTTGAATCTAATTGGGAAGGAGAGAGGTTGCAGAGTGAGGTG
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140
      ATTACACAATAATTACCCAATTAGATTAACCCCTCCCTCTCTCAACGTCTCACTCCAC

      CAGAGCTTGGTGGCAGATGCCAAAGGAATACTGAAACCTTTAGTGTGTCCAGTCTGGAAC
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200
      GTCTCGAACCACTGCTACGGTTCTTATGACTTTGGAATCACACAGGTCAGACCTTG

      TGCATCCAAATTCAGGTTCAAGTAATGATGTCAATTATCCAAACATACCTTCTGTAAATTC
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260
      ACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTTGTATGGAAGACATTTTAAG

      <---- 3.p53-BE ---->
      (promoter)

      ATGCTAAACTACCTAAGAGCTATCTACCGTTCCAAAGCAATAGTGAAGTGTGTT
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320
      TACGATTTGATGGATTCTCGATAGATGGCAAGGTTTCGTTATCACTGAAACTTGTACAA

      CACCAGAGCACGAAAGAATTACAAGATTTTTTTTAAAGAAAATTGGCCAGGAAATAATG
1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380
      GTGGTCTCGTGCTTTCTTAATGTTCTAAAAAAAATTTCTTTTAACCGGTCCTTTATTAC

      AGTAACGAAGGACAGGAAGTAATTGTGAATGTTTAATATAGCTGGGGCTATGCGATTGG
1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
      TCATTGCTTCCTGTCTTCATTAACACTTACAAATTATATCGACCCCGATACGCTAAACC

      CTTAAGTTGTTAGCTTTGTTTTCTCTTGAGAAATAAAACTAAGGGGCCCTCCCTTTTC
1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
      GAATTCACAATCGAAACAAAGGAGAACTCTTTATTTTGAATCCCCGGGAGGGAAG

      AGAGCCTTATGGCGCAACATCTGTACTTTTTCATATGGTTAACTGTCCATTCAGAAACG
1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
      TCTCGGAATACCGCGTTGTAGACATGAAAAAGTATACCAATTGACAGGTAAGGTCTTTGC

      TCTGTGAGCCTCTCATGTTGCAGCCCAACATGGACAGCCCAAGTCAAATGCCCGCAAGT
1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
      AGACACTCGGAGAGTACAACGTCGGTGTGTACCTGTGCGGTCAAGTTACGGGGCGTTCA

      CTTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGCG
1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680
      GAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGGTCCGTCCTGGAGACGC

      CTCTGAGCTCCATTCTCCTTCAAGACCTCCCCAACTCCCAAGGTTGAACTACAGCAGAAG
1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740
      GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTTGAAGGTCCTCACTTGATGTCGTCTTC

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Fig. 10B

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CCTTTAGAAAGGGCAGGAGGCCGGCTCTCGAGGTCCTCACCTGAAGTGAGCATGCCAGCC
1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800
GGAAATCTTTCCCGTCTCCGGCCGAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCGG

ACTGCAGGAACGCCCCGGGACAGGAATGCCCATTTGTGCAACGAACCCCTGACTCCTTCCT
1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860
TGACGTCTTTGCGGGGCCCTGTCTTACGGGTAAACACGTTGCTTGGGACTGAGGAAGGA

CACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGCC
1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920
GTGGGACTGAAGAGGGGGAGGGATGGGCGCGCTCCGGTTCACGACTTAGTTACCTCGG

CTCCCCAACCCGGGCGTTCCCCAGCGAGGCTTCCTTCCCATCCTCTGACCACCGGGGCT
1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980
GAGGGGTTGGGCCCGCAAGGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA

TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTTC
1981 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2040
AAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGCCACAAGTTTCTGCGAAG

TGGGGAGTGAGGGAAGCGGTTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGCACTGG
2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100
ACCCCTCACTCCCTTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCGTGACC

CACGGAACACACCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCCTTCTCTCCCGCG
2101 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160
GTGCCCTTGTGTGGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCGC

GGTTGGTGGACCCGCTCAGTACGGAGTTGGGGAAGCTCTTTCACCTTCGGAGGATTGTCTCA
2161 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220
CCAACCACCTGGGCGAGTCATGCCCTCAACCCCTTCGAGAAAGTGAAGCCTCCTAACGAGT

ACAACCATGCTGGGCATCTGGACCTCCTACCTCTGGTGATCCCTCTCCTGCCCGGGTGG
2221 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280
TGTTGGTACGACCCGTAGACCTGGGAGGATGGAGACCCTAGGGAGAGGACGGGCCACCC

AGGCTTACCCCGTCTTAGTCCCGGGGATAGGCAAGTGGGCGGGCGCGGGACGCGTGCG
2281 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340
TCCGAATGGGGCAGAATCAGGGCCCTATCCGTTTCACCCCGCCCGCGCCCTGCGCACGC

GGATTGCGGGCGGACGCGGCACGCGGGCACCTGGGAGCGCGGGCTGCTGCGGGAGGCG
2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
CCTAACGCCGCCGTGCGCGCGTGCGCCCGTGGACCCCTCGCCGCCCGACGACGCCCTCCGC

TTGGAGACTGGCTCCCGGGGGCTGTTAGGACCTTCCCTCAGGCCCGGGTGCTCAGAACGA
2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
AACCTCTGACCGAGGGCCCCCGACAATCCTGGAAGGGAGTCCGGGCCACGAGCTTGCT

TGGAGGACTTGCTTTTCTTGGGCCTTGATGCGAAGTGCTGATCCCGCTGGGCAGGCGGGG
2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
ACCTCCTGAACGAAAAGAACC CGGAAC TACGCTT CACGACTAGGGCGACCCGTCCGCCCC

CAGCTCCGGCGCTCCTCGGAGACCACTGCGCTCCACGTTGAGGTGGGCGTGGGGGGCGGA
2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
GTCGAGGCCGCGAGGAGCCTCTGGTGACGCGAGGTGCAACTCCACCCGACCCCCGCCT

CAGGAATTGAAGCGGAAGTCTGGGAAGCTTTAGGGTCGCTGGAGGGGGACCCCGGTTGGA
2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
GTCCTTAACCTTCGCTTCAGACCTTCGAAATCCAGCGACCTCCCCCTGGGGCCAACCT

<---- 4.p53-BE ---->
      (intron)

GAGAGGAGCGGAACTCCTGGACAAGCCCTGACAAGCCCAAGCCAAAGGTCCGCTCCGGCGC
2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
CTCTCCTCGCCTTGAGGACCTGTTCCGGACTGTTCCGGTTCGGTTCCAGGCGAGGCCCGC

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Fig. 10C

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GGGTGGGTGAGTGC GCGCCGCCCGGGGGGGGAGAGAGCCTACAGCCTTCAGAACA
2701 -----+-----+-----+-----+-----+ 2760
CCCACCCACTCACGCGCGGGGCGCCCCCGCCCTCTCTCGGATGTCGGAAGTCTTGT

CATATTGCTCATTTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAAGCAGTG
2761 -----+-----+-----+-----+-----+ 2820
GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTTATTTCAGTCGTGGCTTCGTCAC

GTTAAGCCGGAGGGCTCGGAAGAACGGCACCTTTTCTTTCTCGAAAAAGTTATATGGGGG
2821 -----+-----+-----+-----+-----+ 2880
CAATTCGGCCTCCCGAGCCTTCTTGCCGTGGAAGAAAGAGCTTTTCAATATACCCCC

CTGAATGAGCTTCTGGAGGCTTGTTTACCGTTTTTTATTGTACACAGAAAAGGAAACTG
2881 -----+-----+-----+-----+-----+ 2940
GACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAACAGTGTGTCTTTTCCTTTGAC

CCTTGCTCCTTCCGGGAATTCTCTCTTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC
2941 -----+-----+-----+-----+-----+ 3000
GGAACAGAGGGAAGGCCCTTAAGAGAGAAATCTGACATTCAGCGACGGACTCACCAAAG

ATTTTGTGTTGTTTTCTGCCCCTTCTCTTTCTTTTCTTTGCCCCTTCTTAGCTTGCACTCC
3001 -----+-----+-----+-----+-----+ 3060
TAAACAAACAAAAGACGGGAAGAGAAAGAAAGAAACGGGAAGAATCGAACGTGAGG

CATGGTGATTTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTTCCCAACCGCACAGA
3061 -----+-----+-----+-----+-----+ 3120
GTACCACTAAAGACGAACCAGAGGACGCCCAACCACCATGAGCAAGGTTGGCGTGTCT

ACCCGGCGCCTATTATTGGCCAAGAACTTGAGCAGCCTGTTTTGAAAAGTCCCTCGCTC
3121 -----+-----+-----+-----+-----+ 3180
TGGGCGCGGATAATAACCGGTTCTTTGAACTCGTGGACAAAACTTTTCAGGGAGCGAG

AGAAATGCCAGCTTGAGATGGCTAATCAAAG
3181 -----+-----+-----+-----+ 3212
TCTTTACGGTCGAACGTCTACCGATTAGTTTC

```

Fig. 10D

Fig. 11A

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GG AAA AGCCCTGACAAGCCA
	↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2. p1140 IMII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMII	GG AAA AGCCCTG AAA AGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2280 (C→A)

3. p1140 IMIII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIII	GG AAAT CCCTG AAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2273 (G→T)
2280 (C→A)
2283 (G→T)

Fig. 11B

4. p1140 IMIV

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIV	GCACAAGCCCT C ACAAGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2268 (G→T)
2278 (C→A)

Fig. 12A

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GG AAAAT CCCTG AAAAT CCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2. p1141 1p53

p1141	AGAGATGCCCAAAGTGT
p1141 1p53	AGAGAT T CCCAA AAT GTGT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTT
p1141 2p53	AATGTT T CTTAAG A TTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

Fig. 12B

4. p1141 3p53

p1141	AAACTACCTAAGAGCTATCT
p1141 3p53	ACA ATACCTAAGAGCTATCT
	↑ ↑

positions of the mutations (boldface and arrow): 1268 (A→C)
 1270 (C→A)

5. p1141 ΔBgl

	<----- 1.p53-BE ----->
p1141	AATAACCTTT AGAGATGCCCAA ACTGTTTTCCCCAGAACA
p1141ΔBgl	AATAACCTTT A ----- GATCT CCCCAGAACA

6. p1141 ΔSpe

	<----- 2.p53-BE ----->
p1141	CATCTTTGCC AATGTTGCTTAAGCTTTTT GGCTACATTT
p1141ΔBgl	CATCTTTGCC A ----- CTAGT GGCTACATTT

7. p1141 ΔMph

	<----- 3.p53-BE ----->
p1141	AATTCATGCT AAACTACCTAAGAGCTATCT ACCGTTCCAA
p1141ΔBgl	AATTCATGCT ATGCA ----- TACCGTTCCAA

Fig. 13A

variations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
2228 (T→A)

2. p1142 IMIII

p1142	GGACAAGCCCTGACAAGCCA
p1142 IMIII	GG AAA TCCCTG AAA TCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)
2665 (G→T)
2672 (C→A)
2675 (G→T)

3. p1142 ΔBgl

	<---- 1.p53-BE ---->
p1142	AATAACCTTTAGAGATGCCCCAACTGTTTTCCCCAGAACA
p1142ΔBgl	AATAACCTTTA-----GATCTCCCCAGAACA

4. p1142 ΔSpe

	<---- 2.p53-BE ---->
p1142	CATCTTTGCCAATGTTGCTTAAGCTTTTTGGCTACATT
p1142ΔBgl	CATCTTTGCCA-----CTAGTGGCTACATT

[illegible]

5. p1142 Δ Mph

p1142 AATTCATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
 p1142ΔBgl AATTCATGCTATGCA-----TACCGTTCCAA

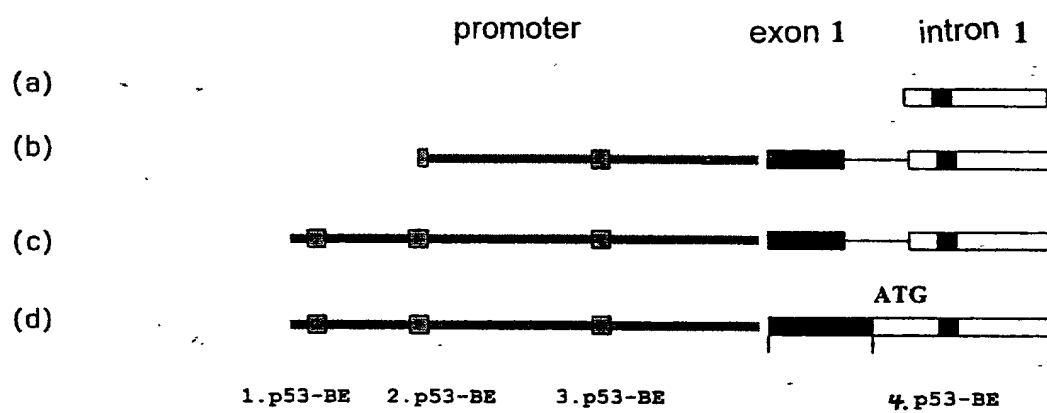


Fig. 14